



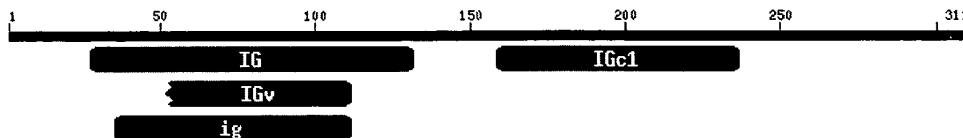
NCBI Conserved Domain Summary

RPS-BLAST 2.2.4 [Aug-26-2002]

Query= gi|1100182|gb|AAA82682.1 T-cell receptor beta [Homo sapiens]
(311 letters)

Database: oasis_sap.v1.58
4540 PSSMs; 885,521 total columns

Click on boxes for multiple alignments



Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D!](#)

PSSMs producing significant alignments:

Score E
(bits) value

- [gnl|CDD|3898](#) smart00407, IGc1, Immunoglobulin C-Type; [77.6](#) 6e-16
- [gnl|CDD|7359](#) smart00409, IG, Immunoglobulin; [44.0](#) 7e-06
- [gnl|CDD|3897](#) smart00406, IGv, Immunoglobulin V-Type; [40.8](#) 7e-05
- [gnl|CDD|7427](#) pfam00047, ig, Immunoglobulin domain. Members of the immunoglo... [39.1](#) 2e-04

- [gnl|CDD|3898](#), smart00407, IGc1, Immunoglobulin C-Type;

CD-Length = 75 residues, 98.7% aligned
Score = 77.6 bits (191), Expect = 6e-16

Query: 158 KATLVCLATGFYPDPHVELSWVWNGKEVHSGVSTDPQLKEQPALNDSRYCLSSRLRVSAT 217
Sbjct: 1 PATLVCLVTGFYPDPDITVTLKNGQEVTSVSTTDPLKDK-----DGTFLSSYLTVSAS 55

Query: 218 FWQNPRNHFRQCQVQFYGLSE 237
Sbjct: 56 TW-ESGDVYTCQVTHEGLTE 74

- [gnl|CDD|7359](#), smart00409, IG, Immunoglobulin;

CD-Length = 86 residues, 100.0% aligned
Score = 44.0 bits (103), Expect = 7e-06

Query: 27 PRHKITKRGQNVTFRCDPIS-EHNRLYWYRQTIGQGPEFLTYFQNEAQLEKSRLLSDRFS 85
Sbjct: 1 PPSVTVKEGESVTLSCASGNPPPEVTWYKQ---GGKLLAY-----SGRFS 43

Query: 86 AERPKGSFSTLEIQRTQGD SAMYLCASSPGTSYEQYFGPGTRLTVT 132
Sbjct: 44 VSRSGGNS-TLTISNVTPEDSGTYCAATN--SSGSASS-GTTLTVL 86

- [gnl|CDD|3897](#), smart00406, IGv, Immunoglobulin V-Type;

CD-Length = 80 residues, only 77.5% aligned
Score = 40.8 bits (95), Expect = 7e-05

Query: 51 LYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAER--PKGSFSTLEIQRTSQGDSAM 108
Sbjct: 18 VSWVRQPPGKGLVGLGYIGSDVSYSEA-SYKGRVTISKDNSKNDV-SLTISNLRVEDTGT 75

Query: 109 YLCA 112
Sbjct: 76 YYCA 79

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- [gnlCDD/7427](#), pfam00047, ig, Immunoglobulin domain. Members of the immunoglobulin superfamily are found in hundreds of proteins of different functions. Examples include antibodies, the giant muscle kinase titin and receptor tyrosine kinases. Immunoglobulin-like domains may be involved in protein-protein and protein-ligand interactions. The Pfam alignments do not include the first and last strand of the immunoglobulin-like domain.

CD-Length = 66 residues, 98.5% aligned
Score = 39.1 bits (90), Expect = 2e-04

Query: 35 GQNVTFRC--DPISEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERP KGS 92
Sbjct: 1 GESVTLTCSVSGYPDPPTVTWLRNGKELELGVLVTS-----SSSGRTSTS 45

Query: 93 FSTLEIQRTSQGDSAMYLCA 112
Sbjct: 46 SLSLTISSVTPEDSGTYTCV 65

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